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IN THE SPECIFICATION

Please amend the paragraph stating on page 3, line 7 and ending at line 9 as follows:

The current invention relates to modified enzymes. Specifically, the invention relates to modified enzymes with improved performance at extreme conditions of pH and temperature. The modification or substitution is numbered from the amino acid after the signal and pro sequence. The signal and pro sequences end at amino acid 33 in SEQ ID NO:1.

Please amend the paragraph starting on page 3, line 10 and ending at line 20 as follows:

In a first aspect, the invention is drawn to a modified xylanase comprising a polypeptide having an amino acid sequence as set forth in SEQ ID NO:1, wherein the sequence has at least one substituted amino acid residue at a position selected from the group consisting of: 2, 5, 7, 10, 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191, wherein the position of the substituted amino acid is numbered from the amino acid after the signal and pro sequence.

Preferably, the substitution is selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191. Preferably, the modified xylanase has at least one substitution selected from the group consisting of: H22K, S65C, N92C, F93W, N97R, V108H, H144C, H144K, F180Q and S186C. Also, preferably, the modified xylanase exhibits improved thermophilicity, alkalophilicity or a combination thereof, in comparison to a wild-type xylanase.

Please amend the paragraph stating on page 14, line 30 and ending at page 15, line 12 as follows:

As used herein, the following designations shall refer to the following mutants:

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"P2" = N97R + H144K / Y5
"P3" = F93W + H144K in Y5
"P8" = F180Q in Y5
"P9" = N97R in F93W + H144K in Y5
"P12" = H144C + N92C in Y5
"P15" = F180Q in H144C + N92C in Y5
"P16" = N97R in H144C + N92C in Y5
"P18" = H22K in Y5
"P20" = H22K + F180Q in Y5
"P21" = H22K + F180Q + H144C + N92C in Y5
"J17" = V108H in Y5
"J21" = S65C + S186C in Y5

wherein position numbering shall be with respect to XynII, wherein the position of the substituted amino acid is numbered from the amino acid after the signal and pro sequence of SEQ ID NO:1.

Please amend the paragraph stating on page 15, line 15 and ending at line 26 as follows:

In a first aspect, the invention is drawn to a modified xylanase comprising a polypeptide having an amino acid sequence as set forth in SEQ ID NO:1, wherein the sequence has at least one substituted amino acid residue at a position selected from the group consisting of: 2, 5, 10, 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191, where position numbering is with respect to SEQ ID NO:1. Preferably, the substitution is selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191. Preferably, the modified xylanase has at least one substitution selected from the group consisting of H22K, S65C, N92C, F93W, N97R, V108H, H144C, H144K, F180Q and S186C. Also, preferably, the modified xylanase exhibits improved thermophilicity, alkalophilicity or a combination thereof, in comparison to a wild-type xylanase, wherein the position of the substituted amino acid is numbered from the amino acid after the signal and pro sequence.